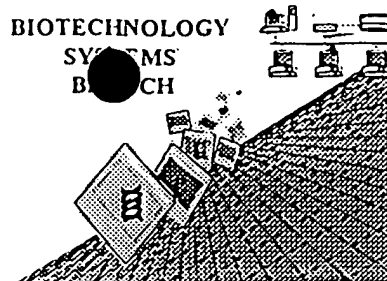


## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/720,560  
Source: PCT09  
Date Processed by STIC: 2-15-2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/720,560

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence.
- 8 ☐ Skipped Sequences      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(x1) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                                 <400> sequence id number  
                                 000
- 10 ☒ Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
                                 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism      Sequence(s) \_\_\_\_\_ are missing this mandatory field or its response.  
(NEW RULES)
- 12 ☒ Use of <220>Feature      Sequence(s) 33 are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
                                 Please explain source of genetic material in <220> to <223> section.  
                                 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

## RAW SEQUENCE LISTING

DATE: 02/15/2001

PATENT APPLICATION: US/09/720,560

TIME: 14:24:04

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\02152001\1720560.raw

4 <110> APPLICANT: American Cyanamid Company  
 5 Fulginiti, James P.  
 6 Fiska, Michael J.  
 7 Dilts, Deborah A.  
 9 <120> TITLE OF INVENTION: NOVEL ANTIGENS OF HELICOBACTER PYLORI  
 12 <130> FILE REFERENCE: 0646/00939  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/720,560  
 C--> 15 <141> CURRENT FILING DATE: 2000-12-21  
 17 <150> PRIOR APPLICATION NUMBER: 60/090,851  
 18 <151> PRIOR FILING DATE: 1998-06-26  
 20 <160> NUMBER OF SEQ ID NOS: 42  
 22 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 708  
 26 <212> TYPE: PR1  
 27 <213> ORGANISM: Helicobacter pylori  
 29 <400> SEQUENCE: 1  
 30 Met Lys Lys Thr Leu Leu Ser Leu Ser Leu Ser Phe Leu  
 31 1 5 10 15  
 32 Leu His Ala Glu Asp Asp Gly Phe Tyr Thr Ser Val Gly Tyr Gln Ile  
 33 20 25 30  
 34 Gly Glu Ala Ala Gln Met Val Lys Asn Thr Lys Gly Ile Gln Glu Leu  
 35 35 40 45  
 36 Ser Asp Asn Tyr Glu Lys Leu Asn Asn Leu Leu Asn Asn Tyr Ser Thr  
 37 50 55 60  
 38 Leu Asn Thr Leu Ile Lys Leu Ser Ala Asp Pro Ser Ala Ile Asn Asp  
 39 65 70 75 80  
 40 Ala Arg Asp Asn Leu Gly Ser Ser Ser Arg Asn Leu Leu Asp Val Lys  
 41 85 90 95  
 42 Thr Asn Ser Pro Ala Tyr Gln Ala Val Leu Leu Ala Leu Asn Ala Ala  
 43 100 105 110  
 44 Val Gly Leu Trp Gln Val Thr Ser Tyr Ala Phe Thr Ala Cys Gly Pro  
 45 115 120 125  
 46 Gly Ser Asn Glu Asn Ala Asn Gly Gly Ile Gln Thr Phe Asn Asn Val  
 47 130 135 140  
 48 Pro Gly Gln Asp Thr Thr Thr Ile Thr Cys Asn Ser Tyr Tyr Glu Pro  
 49 145 150 155 160  
 50 Gly His Gly Gly Pro Ile Ser Thr Ala Asn Tyr Ala Lys Ile Asn Gln  
 51 165 170 175  
 52 Ala Tyr Gln Ile Ile Gln Lys Ala Leu Thr Ala Asn Gly Ala Asn Gly  
 53 180 185 190  
 54 Asp Gly Val Pro Val Leu Ser Asn Thr Thr Thr Lys Leu Asp Phe Thr  
 55 195 200 205  
 56 Ile Asn Gly Asp Lys Arg Thr Gly Gly Lys Pro Asn Thr Pro Glu Lys  
 57 210 215 220  
 58 Phe Pro Trp Ser Asp Gly Lys Tyr Ile His Thr Gln Trp Ile Asn Thr  
 59 225 230 235 240

Does Not Comply  
 Corrected Diskette Needed  
 See Last page

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/720,560

DATE: 02/15/2001  
TIME: 14:24:04

Input Set : A:\Seqlist.txt  
Output Set: N:\CRF3\02152001\I720560.raw

```

60 Ile Val Thr Pro Thr Glu Thr Asn Ile Asn Thr Glu Asn Asn Ala Gln
61                               245                               250                               255
62 Glu Leu Leu Lys Gln Ala Ser Ile Ile Thr Thr Leu Asn Glu Ala
63                               260                               265                               270
64 Cys Pro Asn Phe Gln Asn Gly Gly Arg Ser Tyr Trp Gln Gly Ile Ser
65                               275                               280                               285
66 Gly Asn Gly Thr Met Cys Gly Met Phe Lys Asn Glu Ile Ser Ala Ile
67                               290                               295                               300
68 Gln Gly Met Ile Ala Asn Ala Gln Glu Ala Val Ala Gln Ser Lys Ile
69                               305                               310                               315                               320
70 Val Ser Glu Asn Ala Gln Asn Gln Asn Asn Leu Asp Thr Gly Lys Pro
71                               325                               330                               335
72 Phe Asn Pro Tyr Thr Asp Ala Ser Phe Ala Gln Ser Met Leu Lys Asn
73                               340                               345                               350
74 Ala Gln Ala Gln Ala Glu Ile Leu Asn Gln Ala Glu Gln Val Val Lys
75                               355                               360                               365
76 Asn Phe Glu Lys Ile Pro Thr Ala Phe Val Ser Asp Ser Leu Gly Val
77                               370                               375                               380
78 Cys Tyr Glu Val Gln Gly Gly Glu Arg Arg Gly Thr Asn Pro Gly Gln
79                               385                               390                               395                               400
80 Val Thr Ser Asn Thr Trp Gly Ala Gly Cys Ala Tyr Val Lys Gln Thr
81                               405                               410                               415
82 Ile Thr Asn Leu Asp Asn Ser Ile Ala His Phe Gly Thr Gln Glu Gln
83                               420                               425                               430
84 Gln Ile Gln Gln Ala Glu Asn Ile Ala Asp Thr Leu Val Asn Phe Lys
85                               435                               440                               445
86 Ser Arg Tyr Ser Glu Leu Gly Asn Thr Tyr Asn Ser Ile Thr Thr Ala
87                               450                               455                               460
88 Leu Ser Lys Val Pro Asn Ala Gln Ser Leu Gln Asn Val Val Ser Lys
89                               465                               470                               475                               480
90 Lys Asn Asn Pro Tyr Ser Pro Gln Gly Ile Glu Thr Asn Tyr Tyr Leu
91                               485                               490                               495
92 Asn Gln Asn Ser Tyr Asn Gln Ile Gln Thr Ile Asn Gln Glu Leu Gly
93                               500                               505                               510
94 Arg Asn Pro Phe Arg Lys Val Gly Ile Val Asn Ser Gln Thr Asn Asn
95                               515                               520                               525
96 Gly Ala Met Asn Gly Ile Gly Ile Gln Val Gly Tyr Lys Gln Phe Phe
97                               530                               535                               540
98 Gly Gln Lys Arg Lys Trp Gly Ala Arg Tyr Tyr Gly Phe Phe Asp Tyr
99                               545                               550                               555                               560
100 Asn His Ala Phe Ile Lys Ser Ser Phe Phe Asn Ser Ala Ser Asp Val
101                               565                               570                               575
102 Trp Thr Tyr Gly Phe Gly Ala Asp Ala Leu Tyr Asn Phe Ile Asn Asp
103                               580                               585                               590
104 Lys Ala Thr Asn Phe Leu Gly Lys Asn Asn Lys Leu Ser Val Gly Leu
105                               595                               600                               605
106 Phe Gly Gly Ile Ala Leu Ala Gly Thr Ser Trp Leu Asn Ser Glu Tyr
107                               610                               615                               620
108 Val Asn Leu Ala Thr Val Asn Asn Val Tyr Asn Ala Lys Met Asn Val

```

Input Set : A:\Seqlist.txt  
Output Set: N:\CRF3\02152001\I720560.raw

```

109 625          630          635          640
110 Ala Asn Phe Gln Phe Leu Phe Asn Met Gly Val Arg Met Asn Leu Ala
111          645          650          655
112 Arg Ser Lys Lys Lys Gly Ser Asp His Ala Ala Gln His Gly Ile Glu
113          660          665          670
114 Leu Gly Leu Lys Ile Pro Thr Ile Asn Thr Asn Tyr Tyr Ser Phe Met
115          675          680          685
116 Gly Ala Gln Leu Lys Tyr Arg Arg Leu Tyr Ser Val Tyr Leu Asn Tyr
117          690          695          700
118 Val Phe Ala Tyr
119 705
121 <210> SEQ ID NO: 2
122 <211> LENGTH: 741
123 <212> TYPE: PRT
124 <213> ORGANISM: Helicobacter pylori
126 <400> SEQUENCE: 2
127 Met Lys Lys His Ile Leu Ser Leu Ala Leu Gly Ser Leu Leu Val Ser
128 1 5 10 15
129 Thr Leu Ser Ala Gln Asp Asp Gly Phe Tyr Thr Ser Val Gly Tyr Gln
130 20 25 30
131 Ile Gly Glu Ala Ala Gln Met Val Thr Asn Thr Lys Gly Ile Gln Asp
132 35 40 45
133 Leu Ser Asp Arg Tyr Glu Ser Leu Asn Asn Leu Leu Thr Arg Tyr Ser
134 50 55 60
135 Thr Leu Asn Thr Leu Ile Lys Leu Ser Ala Asp Pro Ser Ala Ile Asn
136 65 70 75 80
137 Ala Ala Arg Glu Asn Leu Gly Ala Ser Ala Lys Asn Leu Ile Gly Asp
138 85 90 95
139 Lys Ala Asn Ser Pro Ala Tyr Gln Ala Val Leu Leu Ala Ile Asn Ala
140 100 105 110
141 Ala Val Gly Phe Trp Asn Val Leu Gly Tyr Ala Thr Gln Cys Gly Gly
142 115 120 125
143 Asn Ala Asn Gly Gln Lys Ser Thr Ser Ser Thr Thr Ile Phe Asn Asn
144 130 135 140
145 Glu Pro Gly Tyr Arg Ser Thr Ser Ile Thr Cys Ser Leu Asn Gly Tyr
146 145 150 155 160
147 Thr Pro Gly Tyr Tyr Gly Pro Met Ser Ile Glu Asn Phe Lys Lys Leu
148 165 170 175
149 Asn Glu Ala Tyr Gln Ile Leu Gln Thr Ala Leu Lys Gln Gly Leu Pro
150 180 185 190
151 Ala Leu Lys Glu Asn Asn Lys Lys Val Asn Val Thr Tyr Thr Tyr Thr
152 195 200 205
153 Cys Ser Gly Gly Gly Asn Asn Asn Cys Ser Ser Gln Ala Thr Gly Val
154 210 215 220
155 Ser Asn Gln Asn Gly Gly Thr Lys Thr Thr Thr Gln Thr Ile Asp Gly
156 225 230 235 240
157 Lys Ser Val Thr Thr Thr Ile Ser Ser Lys Val Val Asp Ser Thr Ala
158 245 250 255
159 Ser Gly Asn Thr Ser Arg Val Ser Tyr Thr Glu Ile Thr Asn Lys Leu

```

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/720,560

DATE: 02/15/2001  
TIME: 14:24:04

Input Set : A:\Seqlist.txt  
Output Set: N:\CRF3\02152001\I720560.raw

160		260		265		270
161	Glu Gly Val	Pro Asp Ser Ala	Gln Ala Leu Leu Ala	Gln Ala Ser Thr		
162		275		280		285
163	Leu Ile Ser Thr	Ile Asn Thr Ala	Cys Pro Phe Phe Ser Val Thr Asn			
164		290		295		300
165	Gln Ser Gly Gly	Pro Gln Met Glu Pro Thr Lys Gly Lys Leu Cys Gly				
166		305		310		315
167	Phe Thr Glu Glu	Ile Ser Ala Ile Gln Lys Met Ile Thr Asp Ala Gln				
168		325		330		335
169	Glu Leu Val Asn	Gln Thr Ser Val Ile Asn Ser His Glu Gln Ser Thr				
170		340		345		350
171	Leu Val Gly Gly	Asn Asn Gly Lys Pro Phe Asn Pro Phe Thr Asp Ala				
172		355		360		365
173	Gln Phe Ala Glu Gly	Met Leu Ala Asn Ala Ser Ala Gln Ala Lys Met				
174		370		375		380
175	Leu Asn Leu Ala His	Gln Val Gly Gln Thr Ile Asn Pro Asn Asn Leu				
176		385		390		395
177	Thr Gly Asn Phe	Lys Asn Phe Val Thr Gly Phe Leu Ala Thr Cys Asn				
178		405		410		415
179	Asn Pro Ser Thr	Ala Gly Thr Gly Gly Thr Gln Gly Ser Ala Pro Gly				
180		420		425		430
181	Thr Val Thr Thr	Gln Thr Phe Ala Ser Gly Cys Ala Tyr Val Glu Gln				
182		435		440		445
183	Thr Ile Thr Asn	Leu Glu Asn Ser Ile Ala His Phe Gly Thr Gln Gln				
184		450		455		460
185	Gln Glu Ile Gln	Arg Ala Glu Asn Ile Ala Asp Thr Leu Val Asn Phe				
186		465		470		475
187	Lys Ser Arg Tyr	Ser Glu Leu Gly Asn Thr Tyr Asn Ser Ile Thr Thr				
188		485		490		495
189	Ala Leu Ser Lys	Val Pro Asn Ala Gln Ser Leu Gln Asn Val Val Ser				
190		500		505		510
191	Lys Lys Asn Asn	Pro Tyr Ser Pro Gln Gly Ile Glu Thr Asn Tyr Tyr				
192		515		520		525
193	Leu Asn Gln Asn	Ser Tyr Asn Gln Ile Gln Thr Ile Asn Gln Glu Leu				
194		530		535		540
195	Gly Arg Asn Pro	Phe Arg Lys Val Gly Ile Val Gly Ser Gln Thr Asn				
196		545		550		555
197	Asn Gly Ala Met	Asn Gly Ile Gly Ile Gln Val Gly Tyr Glu Gln Phe				
198		565		570		575
199	Phe Gly Gln Lys	Arg Lys Trp Gly Ala Arg Tyr Tyr Gly Phe Phe Asp				
200		580		585		590
201	Tyr Asn His Ala	Phe Ile Lys Ser Ser Phe Phe Asn Ser Ala Ser Asp				
202		595		600		605
203	Val Trp Thr Tyr	Gly Phe Gly Ala Asp Ala Leu Tyr Asn Phe Ile Asn				
204		610		615		620
205	Asp Lys Ala Thr	Asn Phe Leu Gly Lys Asn Asn Lys Leu Ser Val Gly				
206		625		630		635
207	Leu Phe Gly Gly	Ile Ala Leu Ala Gly Thr Ser Trp Leu Asn Ser Glu				
208		645		650		655

## RAW SEQUENCE LISTING

DATE: 02/15/2001

PATENT APPLICATION: US/09/720,560

TIME: 14:24:04

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\02152001\I720560.raw

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209 Tyr Val Asn Leu Ala Thr Val Asn Asn Val Tyr Asn Ala Lys Met Asn
210                      660                      665                      670
211 Val Ala Asn Phe Gln Phe Leu Phe Asn Met Gly Val Arg Met Asn Leu
212                      675                      680                      685
213 Ala Arg Pro Lys Lys Asn Asp Ser Asp His Ala Ala Gln His Gly Ile
214                      690                      695                      700
215 Gln Leu Gly Leu Lys Ile Pro Thr Ile Asn Thr Asn Tyr Tyr Ser Phe
216                      705                      710                      715                      720
217 Met Gly Ala Glu Leu Lys Tyr Arg Arg Leu Tyr Ser Val Tyr Leu Asn
218                      725                      730                      735
219 Tyr Val Phe Ala Tyr
220                      740
221 <210> SEQ_ID NO: 3
222 <211> LENGTH: 745
223 <212> TYPE: PRT
224 <213> ORGANISM: Helicobacter pylori
225 <400> SEQUENCE: 3
228 Met Lys Lys His Ile Leu Ser Leu Ala Leu Gly Ser Leu Leu Val Ser
229 1 5 10 15
230 Thr Leu Ser Ala Glu Asp Asp Gly Phe Tyr Thr Ser Val Gly Tyr Gln
231 20 25 30
232 Ile Gly Glu Ala Ala Gln Met Val Thr Asn Thr Lys Gly Ile Gln Gln
233 35 40 45
234 Leu Ser Asp Asn Tyr Glu Asn Leu Asn Asn Leu Leu Thr Arg Tyr Ser
235 50 55 60
236 Thr Leu Asn Thr Leu Ile Lys Leu Ser Ala Asp Pro Ser Ala Ile Asn
237 65 70 75 80
238 Ala Val Arg Glu Asn Leu Gly Ala Ser Thr Lys Asn Leu Ile Gly Asp
239 85 90 95
240 Lys Ala Asn Ser Pro Ala Tyr Gln Ala Val Phe Leu Ala Ile Asn Ala
241 100 105 110
242 Ala Val Gly Leu Trp Asn Phe Ile Gly Tyr Ala Val Met Cys Gly Asn
243 115 120 125
244 Gly Asn Gly Thr Glu Ser Gly Pro Gly Ser Val Ile Phe Asn Asp Gln
245 130 135 140
246 Pro Gly Gln Asp Ser Thr Gln Ile Thr Cys Asn Arg Phe Glu Ser Thr
247 145 150 155 160
248 Gly Pro Gly Lys Ser Met Ser Ile Asp Gln Phe Lys Lys Leu Asn Glu
249 165 170 175
250 Ala Tyr Gln Ile Ile Gln Gln Ala Leu Lys Asn Gln Ser Gly Phe Pro
251 180 185 190
252 Gln Leu Gly Gly Asn Gly Thr Lys Val Ser Val Asn Tyr Asn Tyr Gln
253 195 200 205
254 Cys Arg Gln Thr Ala Asp Ile Asn Gly Gly Val Tyr Gln Phe Cys Lys
255 210 215 220
256 Ala Lys Asn Gly Ser Ser Ser Ser Ser Asn Gly Gly Asn Gly Ser Ser
257 225 230 235 240
258 Thr Gln Thr Thr Ala Thr Thr Thr Gln Asp Gly Val Thr Ile Thr Thr
259 245 250 255

```

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/720,560

DATE: 02/15/2001  
TIME: 14:24:05

Input Set : A:\Seqlist.txt  
Output Set: N:\CRF3\02152001\I720560.raw

L:14 M:270 C: Current Application Number differs. Replaced Current Application Number  
L:15 M:271 C: Current Filing Date differs. Replaced Current Filing Date  
L:935 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:935 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:936 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:33  
L:936 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:33  
L:936 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:33

ATI



<211> 16  
<212> PRT  
<213> Helicobacter pylori

<400> 31  
Cys Leu Val Arg Ser Thr Asn Asn Glu Asn Thr Pro Gly Gly Gly Gln  
1 5 10 15

<210> 32  
<211> 14  
<212> PRT  
<213> Helicobacter pylori

<400> 32  
Cys Arg Gln Thr Ala Asp Ile Asn Gly Gly Val Tyr Gln Phe  
1 5 10

<210> 33  
<211> 60  
<212> DNA  
<213> "Artificial Sequence"

*requires use of numeric identifiers 22207 and 22217  
see item 12 on error summary sheet.*

<400> 33  
gargaygayg gnttytayac gwshtyggg taycarathg gngargcngc gcaratggtn 60

*requires use of numeric  
identifiers 22207, 22217,  
22227, and  
22237*

<210> 34  
<211> 20  
<212> PRT  
<213> Helicobacter pylori

*see item 10 on  
error summary sheet*

<400> 34  
Glu Asp Asp Gly Phe Tyr Thr Ser Val Gly Tyr Gln Ile Gly Glu Ala  
1 5 10 15  
Ala Gln Met Val  
20

<210> 35  
<211> 21  
<212> PRT  
<213> Helicobacter pylori

<400> 35  
Glu Asp Asp Gly Phe Tyr Thr Ser Val Gly Tyr Gln Ile Gly Glu Ala  
1 5 10 15  
Ala Gln Met Val Lys  
20

<210> 36  
<211> 15  
<212> PRT  
<213> Helicobacter pylori

<400> 36  
Ser Thr Ser Ser Thr Thr Ile Phe Asn Asn Glu Pro Gly Tyr Arg  
1 5 10 15

<210> 37